

SEQ SEARCH RESULTS

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 7, 2004, 00:04:05 ; Search time 3237 Seconds
(without alignments)
9814.780 Million cell updates/sec

Title: US-09-449-817A-1
Perfect score: 733
Sequence: 1 tacgacttggtcaacctggc.....ctaaaaaaaaaaaaaaaaaaaaa 733

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query		DB		ID	Description
No.	Score	Match	Length					
1	712.4	97.2	1766	9	BC042150	GenBank 2003	BC042150	Homo sapi
2	699.4	95.4	1845	9	AY029585	GB 2001	AY029585	Homo sapi
3	699.4	95.4	3098	6	BD270075	GB 2002	BD270075	Secreted
4	699.4	95.4	3844	6	AX211372	GB 2001	AX211372	Sequence
5	699.4	95.4	3912	6	AX877306	GB 2003	AX877306	Sequence
6	699.4	95.4	3912	6	BD156590	GB 2003	BD156590	Primer fo
7	699.4	95.4	3912	9	AK001691	GB 2000	AK001691	Homo sapi
8	699.4	95.4	3912	9	AY214461	GB 2003	AY214461	Homo sapi
9	697.8	95.2	4273	9	HSM806216	GB 2003	BX538047	Homo sapi
10	697.8	95.2	4305	9	HSM804937	GB 2003	AL833624	Homo sapi
11	694.4	94.7	1720	6	AX470187	GB 2002	AX470187	Sequence
12	683.4	93.2	1884	9	AY082673	GB 2002	AY082673	Homo sapi
13	683.4	93.2	1886	9	AF238864	GB 2000	AF238864	Homo sapi
14	541.4	73.9	2824	6	AX883606		AX883606	Sequence
15	541.4	73.9	2824	6	BD160421		BD160421	Primer fo
16	541.4	73.9	2824	9	AK024163		AK024163	Homo sapi
17	509.4	69.5	2118	9	AF262322		AF262322	Homo sapi
18	509	69.4	149884	9	AC016736		AC016736	Homo sapi
19	500	68.2	742	6	AX866662		AX866662	Sequence
20	500	68.2	742	6	BD146724		BD146724	Primer fo
21	381.4	52.0	1760	10	BC037435		BC037435	Mus muscu
22	375.8	51.3	2969	6	AX470185		AX470185	Sequence
23	375.8	51.3	2969	10	AY214462		AY214462	Mus muscu
24	357.8	48.8	2706	10	AF238865		AF238865	Rattus no
25	357.8	48.8	2707	10	AF335281		AF335281	Rattus no
26	354	48.3	1971	10	AY029586		AY029586	Mus muscu
27	309.2	42.2	401	6	BD232193		BD232193	Novel ser
28	309.2	42.2	401	6	AR366789		AR366789	Sequence
29	309.2	42.2	401	6	AX155256		AX155256	Sequence
c 30	289	39.4	1203	6	A63553		A63553	Sequence 6
c 31	289	39.4	1203	6	AR271262		AR271262	Sequence
c 32	256.6	35.0	63358	2	AC073448		AC073448	Homo sapi
33	226	30.8	160207	2	AC130700		AC130700	Mus muscu

OM nucleic - nucleic search, using sw model

Run on: June 7, 2004, 06:33:16 ; Search time 745 Seconds
(without alignments)
4179.771 Million cell updates/sec

Title: US-09-449-817A-1
Perfect score: 733
Sequence: 1 tacgacttggtcaacctggc.....ctaaaaaaaaaaaaaaaaaaaaa 733

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	% Query Match	Length	DB	ID	Description
1	699.4	95.4	1169	5	AAS08645	Aas08645 Human cDN
2	699.4	95.4	1169	7	ABX91940	Abx91940 Human G p
3	699.4	95.4	2936	5	AAS08646	Aas08646 Human cDN
4	699.4	95.4	2936	7	ABX91941	Abx91941 Human G p
5	699.4	95.4	3098	3	AAA23459	Aaa23459 cDNA enco
6	699.4	95.4	3844	4	AAH76202	Aah76202 Human dru
7	699.4	95.4	3910	5	AAS15815	Aas15815 Human cDN
8	699.4	95.4	3912	4	AAH14598	Aah14598 Human cDN

40 01/53454
7/2001
FD 12/22/00
68-2003
11-2004 22000
≥ 2000
≥ 2000
40 2000/11015
printed no pending US
2 2000
only JP 1999

9	694.4	94.7	1720	6	ABN85027	Z 2000	Abn85027	Human	Tum
10	683.4	93.2	1886	4	AAC89165	Z 2000	Aac89165	Human	p-H
11	662.6	90.4	1038	4	AAF91864	W0 00/71564	Aaf91864	Human	sec
12	662.6	90.4	1038	7	ADA56557	Z 2001	Ada56557	Gene	enco
13	541.4	73.9	2824	4	AAH18429		Aah18429	Human	cDN
14	509.4	69.5	2118	4	AAC89166		Aac89166	Human	p-H
15	500	68.2	742	4	AAH04732		Aah04732	Human	cDN
16	461.2	62.9	774	7	ADA56119		Ada56119	Gene	enco
17	458.6	62.6	1467	7	ABX91942		Abx91942	Human	G p
18	390.2	53.2	449	8	ACH36377		Ach36377	Human	end
19	388	52.9	474	8	ACH43626		Ach43626	Human	foe
20	375.8	51.3	2969	6	ABN85026		Abn85026	Murine	Tu
21	357.8	48.8	2714	4	AAC89167		Aac89167	Rat	p-HYD
22	357.8	48.8	3885	4	AAC89169		Aac89169	AdRSVp	PHYD
23	309.2	42.2	401	3	AAZ49402		Aaz49402	Human	pla
24	309.2	42.2	401	5	AAD07077		Aad07077	Placental	
c 25	289	39.4	1203	2	AAT64815		Aat64815	Tumour	su
26	125.8	17.2	1680	5	AAS15802		Aas15802	Human	cDN
27	125.8	17.2	1891	6	AAD46429		Aad46429	Human	STE
28	125.8	17.2	1891	8	ACD27642		Acd27642	cDNA	enco
29	125.8	17.2	4329	5	AAS15801		Aas15801	Human	ORF
30	107.4	14.7	1198	2	AAV80586		Aav80586	Kidney	in
31	107.4	14.7	1213	3	AAZ46296		Aaz46296	Human	pro
32	107.4	14.7	1365	6	ABK92252		Abk92252	Prostate	
33	107.4	14.7	1403	7	ACC95737		Acc95737	Prostate	
34	107.4	14.7	1403	9	ADB14445		Adb14445	Human	pro
35	107.4	14.7	1561	5	AAS15811		Aas15811	Human	cDN
36	107.4	14.7	2238	5	AAS15810		Aas15810	Human	ORF
37	107.4	14.7	2283	6	ABK11093		Abk11093	cDNA	enco
38	107.4	14.7	2283	6	ABK50391		Abk50391	Human	cDN
39	107.4	14.7	2283	8	ACD25893		Acd25893	Tumour	-as
40	107.4	14.7	2453	5	AAD07072		Aad07072	Human	six
41	107.4	14.7	2469	9	ADB63031		Adb63031	Human	cDN
42	103.8	14.2	391	5	AAS11983		Aas11983	Human	cDN
43	103.8	14.2	391	7	ABX91939		Abx91939	Human	G p
44	101	13.8	434	6	ABK92428		Abk92428	Human	pro
45	100	13.6	354	6	ABK50400		Abk50400	Human	PUM

Steiner
et al.

ALIGNMENTS

RESULT 1

AAS08645

ID AAS08645 standard; cDNA; 1169 BP.

XX

AC AAS08645;

XX

DT 17-DEC-2001 (first entry)

XX

DE Human cDNA encoding G-protein coupled receptor like protein, GPCR #3.

XX

KW Human; G-protein coupled receptor like protein; GPCR; immunogen;

KW ophthalmic disease; neurological disease; Alzheimer's disease;

KW Parkinson's disease; immunological disorder; HIV; candidiasis;

KW human immunodeficiency virus; autoimmune disorder; multiple sclerosis;

KW systemic lupus erythematosus; rheumatoid arthritis; platelet disorder;

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OM nucleic - nucleic search, using sw model

Run on: June 7, 2004, 06:50:16 ; Search time 397 Seconds
(without alignments)
8423.030 Million cell updates/sec

Title: US-09-449-817A-1
Perfect score: 733
Sequence: 1 tacgacttggtcaacctggc.....ctaaaaaaaaaaaaaaaaaaaaa 733

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2995936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters: 5991872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	699.4	95.4	1169	9	US-09-747-835A-11	Sequence 11, Appl
2	699.4	95.4	1169	13	US-10-312-312-11	Sequence 11, Appl
3	699.4	95.4	2936	9	US-09-747-835A-12	Sequence 12, Appl
4	699.4	95.4	2936	13	US-10-312-312-12	Sequence 12, Appl
5	699.4	95.4	3844	15	US-10-182-951-18	Sequence 18, Appl
6	699.4	95.4	3910	16	US-10-239-607-35	Sequence 35, Appl
7	699.4	95.4	3912	13	US-10-342-887-1763	Sequence 1763, Ap
8	699.4	95.4	3912	13	US-10-172-118-1763	Sequence 1763, Ap
9	662.6	90.4	1038	9	US-09-789-561-17 ACT	Sequence 17, Appl
10	458.6	62.6	1467	9	US-09-747-835A-14	Sequence 14, Appl
11	458.6	62.6	1467	13	US-10-312-312-14	Sequence 14, Appl
12	390.2	53.2	449	10	US-09-918-995-23589	Sequence 23589, A
13	388	52.9	474	10	US-09-918-995-30838	Sequence 30838, A
14	309.2	42.2	401	12	US-10-408-009-12	Sequence 12, Appl
15	309.2	42.2	401	15	US-10-011-095-12	Sequence 12, Appl
16	309.2	42.2	401	15	US-10-010-667A-12	Sequence 12, Appl
17	309.2	42.2	401	15	US-10-165-044-14	Sequence 14, Appl
18	125.8	17.2	1680	16	US-10-239-607-23	Sequence 23, Appl
19	125.8	17.2	1891	9	US-09-802-520-2	Sequence 2, Appli
20	125.8	17.2	1891	13	US-10-205-267-2	Sequence 2, Appli
21	125.8	17.2	3754	13	US-10-455-822-12	Sequence 12, Appl
22	125.8	17.2	3754	13	US-10-455-822-175	Sequence 175, App
23	125.8	17.2	3754	13	US-10-455-822-177	Sequence 177, App
24	125.8	17.2	4329	16	US-10-239-607-22	Sequence 22, Appl
25	125.8	17.2	6857	13	US-10-455-822-16	Sequence 16, Appl
26	125.8	17.2	6857	13	US-10-455-822-52	Sequence 52, Appl
27	125.8	17.2	6857	13	US-10-455-822-54	Sequence 54, Appl
28	125.8	17.2	6857	13	US-10-455-822-56	Sequence 56, Appl
29	125.8	17.2	6857	13	US-10-455-822-58	Sequence 58, Appl
30	125.8	17.2	6857	13	US-10-455-822-60	Sequence 60, Appl
31	125.8	17.2	6857	13	US-10-455-822-62	Sequence 62, Appl
32	125.8	17.2	6857	13	US-10-455-822-64	Sequence 64, Appl
33	125.8	17.2	6857	13	US-10-455-822-66	Sequence 66, Appl
34	125.8	17.2	6857	13	US-10-455-822-68	Sequence 68, Appl
35	125.8	17.2	6857	13	US-10-455-822-70	Sequence 70, Appl
36	125.8	17.2	6857	13	US-10-455-822-72	Sequence 72, Appl
37	125.8	17.2	6857	13	US-10-455-822-74	Sequence 74, Appl
38	125.8	17.2	6857	13	US-10-455-822-76	Sequence 76, Appl
39	125.8	17.2	6857	13	US-10-455-822-187	Sequence 187, App
40	125.8	17.2	6857	13	US-10-455-822-189	Sequence 189, App
41	124.2	16.9	6857	13	US-10-455-822-50	Sequence 50, Appl
42	107.4	14.7	1213	9	US-09-963-896-3	Sequence 3, Appli
43	107.4	14.7	1365	16	US-10-295-027-573	Sequence 573, App
44	107.4	14.7	1403	14	US-10-012-896-995	Sequence 995, App
45	107.4	14.7	1403	15	US-10-144-678A-995	Sequence 995, App

ALIGNMENTS

RESULT 1
US-09-747-835A-11

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OM nucleic - nucleic search, using sw model

Run on: June 7, 2004, 06:25:20 ; Search time 2546 Seconds
(without alignments)
8597.399 Million cell updates/sec

Title: US-09-449-817A-1
Perfect score: 733
Sequence: 1 tacgacttggtcaacctggc.....ctaaaaaaaaaaaaaaaaaaaaa 733

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	677.6	92.4	862	13	BQ721171	BQ721171 AGENCOURT
c	2	639.4	87.2	670	12	BM677810	BM677810 UI-E-EJ0-
c	3	624	85.1	644	13	BQ448110	BQ448110 UI-H-EU1-
c	4	621.2	84.7	1111	9	AL577999	AL577999 AL577999
	5	584.6	79.8	924	13	BX410099	BX410099 BX410099
	6	576.4	78.6	600	12	BM725382	BM725382 UI-E-EJ0-
c	7	547.2	74.7	896	13	BX436148	BX436148 BX436148
c	8	520.8	71.1	554	10	BE207855	BE207855 bb06d06.x
	9	500	68.2	742	9	AU121735	AU121735 AU121735
	10	430.2	58.7	1467	29	AY407187	AY407187 Homo sapi
	11	424.6	57.9	668	12	BM734828	BM734828 MON01_13
	12	422.8	57.7	900	13	BQ948163	BQ948163 AGENCOURT
c	13	392	53.5	409	9	AI872457	AI872457 ty41g09.x
	14	381.4	52.0	1742	11	BC027251	BC027251 Mus muscu
	15	376.8	51.4	2728	11	AK028961	AK028961 Mus muscu
	16	375.8	51.3	2933	11	AK078769	AK078769 Mus muscu
	17	347.4	47.4	692	13	BY756731	BY756731 BY756731
	18	338.6	46.2	794	9	AU124448	AU124448 AU124448
c	19	324.2	44.2	329	9	AI206292	AI206292 qr26f06.x
	20	313.4	42.8	1219	29	AY407189	AY407189 Mus muscu
	21	309.2	42.2	401	14	R80991	R80991 yi94c03.r1
c	22	288.8	39.4	650	10	AW226598	AW226598 up09h09.x
c	23	257.4	35.1	652	10	AW226592	AW226592 up09g09.x
c	24	251	34.2	642	10	AW226573	AW226573 up09e09.x
	25	227	31.0	778	10	BF135381	BF135381 601783468
c	26	217.2	29.6	383	13	C82712	C82712 C82712 rabb
	27	217.2	29.6	383	13	C83568	C83568 C83568 rabb
	28	216.4	29.5	928	13	BU222579	BU222579 603108070
	29	212	28.9	576	12	BG689640	BG689640 337800 BA
	30	211.4	28.8	423	10	BF563520	BF563520 UI-R-C4-a
	31	206.8	28.2	900	13	BU404224	BU404224 603483796
	32	206	28.1	524	10	BF152301	BF152301 uz31e08.y
	33	200.8	27.4	1467	29	AY407188	AY407188 Pan trogl
	34	187.6	25.6	644	14	CA343411	CA343411 673507 NC
	35	185.6	25.3	241	12	BG951363	BG951363 MR1-CT073
	36	173.8	23.7	341	9	AA223534	AA223534 zr07c10.r
	37	170.4	23.2	675	10	BE380978	BE380978 601271515
	38	156	21.3	1287	11	AK003108	AK003108 Mus muscu
	39	154.2	21.0	1503	29	AY402677	AY402677 Mus muscu
	40	154.2	21.0	3403	11	AK052981	AK052981 Mus muscu
	41	153.2	20.9	907	14	CA488941	CA488941 AGENCOURT
	42	152.6	20.8	4265	11	AK086787	AK086787 Mus muscu
	43	150.4	20.5	833	13	BU563157	BU563157 AGENCOURT
	44	150	20.5	417	10	BB810801	BB810801 BB810801
	45	148.6	20.3	1586	11	BC043459	BC043459 Mus muscu

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 7, 2004, 08:31:00 ; Search time 6207 Seconds
(without alignments)
1298.825 Million cell updates/sec

Title: US-09-449-817A-2
Perfect score: 1008
Sequence: 1 MEIYLSLGLVLA LGTSL LLA V.....QIGGLRSKFLGLKCMHDYSE 186

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09449817/runat_03062004_144647_22281/app_query.fasta_1.3
27

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09449817@CGN_1_1_3508@runat_03062004_144647_22281 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*

11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*
 15: em_ba:*
 16: em_fun:*
 17: em_hum:*
 18: em_in:*
 19: em_mu:*
 20: em_om:*
 21: em_or:*
 22: em_ov:*
 23: em_pat:*
 24: em_ph:*
 25: em_pl:*
 26: em_ro:*
 27: em_sts:*
 28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

At least Thu 66
 is a mismatch to SEQ 2
 (also an extra bp)

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	974	96.6	1720	6	AX470187	AX470187 Sequence
2	974	96.6	1766	9	BC042150	BC042150 Homo sapi
3	974	96.6	1845	9	AY029585	AY029585 Homo sapi
4	974	96.6	1884	9	AY082673	AY082673 Homo sapi
5	974	96.6	1886	9	AF238864	AF238864 Homo sapi
6	974	96.6	3098	6	BD270075	BD270075 Secreted
7	974	96.6	3844	6	AX211372	AX211372 Sequence
8	974	96.6	3912	6	AX877306	AX877306 Sequence
9	974	96.6	3912	6	BD156590	BD156590 Primer fo
10	974	96.6	3912	9	AK001691	AK001691 Homo sapi
11	974	96.6	3912	9	AY214461	AY214461 Homo sapi
12	974	96.6	4305	9	HSM804937	AL833624 Homo sapi
13	969	96.1	4273	9	HSM806216	BX538047 Homo sapi
14	907.5	90.0	2118	9	AF262322	AF262322 Homo sapi
15	793.5	78.7	2824	6	AX883606	AX883606 Sequence
16	793.5	78.7	2824	6	BD160421	BD160421 Primer fo

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 7, 2004, 07:35:57 ; Search time 369 Seconds
(without alignments)
2141.368 Million cell updates/sec

Title: US-09-449-817A-2
Perfect score: 1008
Sequence: 1 MEIYLSLGLVLAALGTLALLAV.....QIGGLRSKFLGLKCMHDYSE 186

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09449817/runat_03062004_144647_22273/app_query.fasta_1.3
27

-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09449817_@CGN_1_1_470 @runat_03062004_144647_22273 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query		DB	ID	Description
	No.	Score			
	1	974	96.6	1038	4 AAF91864 Aaf91864 Human sec
	2	974	96.6	1038	7 ADA56557 Ada56557 Gene enco
	3	974	96.6	1169	5 AAS08645 Aas08645 Human cDN
	4	974	96.6	1169	7 ABX91940 Abx91940 Human G p
	5	974	96.6	1720	6 ABN85027 Abn85027 Human Tum
	6	974	96.6	1886	4 AAC89165 Aac89165 Human p-H
	7	974	96.6	2936	5 AAS08646 Aas08646 Human cDN
	8	974	96.6	2936	7 ABX91941 Abx91941 Human G p
	9	974	96.6	3098	3 AAA23459 Aaa23459 cDNA enco
	10	974	96.6	3844	4 AAH76202 Aah76202 Human dru
	11	974	96.6	3910	5 AAS15815 Aas15815 Human cDN
	12	974	96.6	3912	4 AAH14598 Aah14598 Human cDN
	13	907.5	90.0	2118	4 AAC89166 Aac89166 Human p-H
	14	793.5	78.7	2824	4 AAH18429 Aah18429 Human cDN
	15	780.5	77.4	742	4 AAH04732 Aah04732 Human cDN
	16	742.5	73.7	774	7 ADA56119 Ada56119 Gene enco
	17	713	70.7	449	8 ACH36377 Ach36377 Human end
	18	688	68.3	1467	7 ABX91942 Abx91942 Human G p
	19	570	56.5	474	8 ACH43626 Ach43626 Human foe
	20	557.5	55.3	2714	4 AAC89167 Aac89167 Rat p-HYD
	21	557.5	55.3	3885	4 AAC89169 Aac89169 AdRSVpHYD
	22	528.5	52.4	2969	6 ABN85026 Abn85026 Murine Tu
c	23	445	44.1	1203	2 AAT64815 Aat64815 Tumour su
	24	420	41.7	401	3 AAZ49402 Aaz49402 Human pla
	25	420	41.7	401	5 AAD07077 Aad07077 Placental
	26	254	25.2	354	6 ABK50400 Abk50400 Human PUM
	27	254	25.2	1213	3 AAZ46296 Aaz46296 Human pro
	28	254	25.2	1365	6 ABK92252 Abk92252 Prostate
	29	254	25.2	1403	7 ACC95737 Acc95737 Prostate
	30	254	25.2	1403	9 ADB14445 Adb14445 Human pro
	31	254	25.2	1561	5 AAS15811 Aas15811 Human cDN
	32	254	25.2	1680	5 AAS15802 Aas15802 Human cDN
	33	254	25.2	1891	6 AAD46429 Aad46429 Human STE
	34	254	25.2	1891	8 ACD27642 Acd27642 cDNA enco
	35	254	25.2	2238	5 AAS15810 Aas15810 Human ORF
	36	254	25.2	2283	6 ABK11093 Abk11093 cDNA enco
	37	254	25.2	2283	6 ABK50391 Abk50391 Human cDN
	38	254	25.2	2283	8 ACD25893 Acd25893 Tumour-as
	39	254	25.2	2453	5 AAD07072 Aad07072 Human six
	40	254	25.2	2469	9 ADB63031 Adb63031 Human cDN
	41	254	25.2	4329	5 AAS15801 Aas15801 Human ORF
c	42	249.5	24.8	739	8 ACD27821 Acd27821 Human tra
	43	249	24.7	434	6 ABK92428 Abk92428 Human pro
	44	238	23.6	519	3 AAZ49398 Aaz49398 Human STR
	45	225.5	22.4	1725	5 AAS15793 Aas15793 Human DNA

ALIGNMENTS

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 7, 2004, 09:26:11 ; Search time 385 Seconds
(without alignments)
2203.977 Million cell updates/sec

Title: US-09-449-817A-2
Perfect score: 1008
Sequence: 1 MEIYLSLGLVLA LGTSL LAV.....QIGGLRSKFLGLKCMHDYSE 186

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2995936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters: 5991872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09449817/runat_03062004_144648_22301/app_query.fasta_1.3
27

-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09449817 @CGN 1 1 221 @runat_03062004_144648_22301
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	974	96.6	1038	9	US-09-789-561-17	Sequence 17, Appl
2	974	96.6	1169	9	US-09-747-835A-11	Sequence 11, Appl
3	974	96.6	1169	13	US-10-312-312-11	Sequence 11, Appl
4	974	96.6	2936	9	US-09-747-835A-12	Sequence 12, Appl
5	974	96.6	2936	13	US-10-312-312-12	Sequence 12, Appl
6	974	96.6	3844	15	US-10-182-951-18	Sequence 18, Appl
7	974	96.6	3910	16	US-10-239-607-35	Sequence 35, Appl
8	974	96.6	3912	13	US-10-342-887-1763	Sequence 1763, Ap
9	974	96.6	3912	13	US-10-172-118-1763	Sequence 1763, Ap
10	713	70.7	449	10	US-09-918-995-23589	Sequence 23589, A
11	688	68.3	1467	9	US-09-747-835A-14	Sequence 14, Appl
12	688	68.3	1467	13	US-10-312-312-14	Sequence 14, Appl
13	570	56.5	474	10	US-09-918-995-30838	Sequence 30838, A
14	420	41.7	401	12	US-10-408-009-12	Sequence 12, Appl
15	420	41.7	401	15	US-10-011-095-12	Sequence 12, Appl
16	420	41.7	401	15	US-10-010-667A-12	Sequence 12, Appl
17	420	41.7	401	15	US-10-165-044-14	Sequence 14, Appl
18	254	25.2	354	16	US-10-392-190-11	Sequence 11, Appl
19	254	25.2	1213	9	US-09-963-896-3	Sequence 3, Appli
20	254	25.2	1365	16	US-10-295-027-573	Sequence 573, App
21	254	25.2	1403	14	US-10-012-896-995	Sequence 995, App
22	254	25.2	1403	15	US-10-144-678A-995	Sequence 995, App
23	254	25.2	1403	15	US-10-294-025-995	Sequence 995, App
24	254	25.2	1561	16	US-10-239-607-28	Sequence 28, Appl
25	254	25.2	1680	16	US-10-239-607-23	Sequence 23, Appl
26	254	25.2	1891	9	US-09-802-520-2	Sequence 2, Appli
27	254	25.2	1891	13	US-10-205-267-2	Sequence 2, Appli
28	254	25.2	2238	16	US-10-239-607-27	Sequence 27, Appl
29	254	25.2	2280	13	US-10-455-822-6	Sequence 6, Appli
30	254	25.2	2280	13	US-10-455-822-157	Sequence 157, App
31	254	25.2	2280	13	US-10-455-822-159	Sequence 159, App
32	254	25.2	2283	10	US-09-888-257A-5	Sequence 5, Appli
33	254	25.2	2283	16	US-10-392-190-1	Sequence 1, Appli
34	254	25.2	2374	13	US-10-455-822-8	Sequence 8, Appli
35	254	25.2	2374	13	US-10-455-822-163	Sequence 163, App
36	254	25.2	2374	13	US-10-455-822-165	Sequence 165, App
37	254	25.2	2453	12	US-10-408-009-5	Sequence 5, Appli
38	254	25.2	2453	13	US-10-455-822-2	Sequence 2, Appli
39	254	25.2	2453	13	US-10-455-822-18	Sequence 18, Appl

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 7, 2004, 09:13:41 ; Search time 2364 Seconds
(without alignments)
2349.562 Million cell updates/sec

Title: US-09-449-817A-2
Perfect score: 1008
Sequence: 1 MEIYLSLGVLALGTLSELLAV.....QIGGLRSKFLGLKCMHDYSE 186

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09449817/runat_03062004_144648_22291/app_query.fasta_1.3
27

-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09449817@CGN_1_1_2810@runat_03062004_144648_22291 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*

12: gb_est3:*
 13: gb_est4:*
 14: gb_est5:*
 15: em_estfun:*
 16: em_estom:*
 17: em_gss_hum:*
 18: em_gss_inv:*
 19: em_gss_pln:*
 20: em_gss_vrt:*
 21: em_gss_fun:*
 22: em_gss_mam:*
 23: em_gss_mus:*
 24: em_gss_pro:*
 25: em_gss_rod:*
 26: em_gss_phg:*
 27: em_gss_vrl:*
 28: gb_gss1:*
 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result	%						Description
	No.	Score	Query Match	Length	DB	ID	
c	1	974	96.6	670	12	BM677810	BM677810 UI-E-EJ0-
	2	974	96.6	862	13	BQ721171	BQ721171 AGENCOURT
	3	961	95.3	600	12	BM725382	BM725382 UI-E-EJ0-
c	4	953	94.5	644	13	BQ448110	BQ448110 UI-H-EU1-
c	5	908	90.1	1111	9	AL577999	AL577999 AL577999
	6	894.5	88.7	924	13	BX410099	BX410099 BX410099
c	7	845	83.8	896	13	BX436148	BX436148 BX436148
c	8	807	80.1	554	10	BE207855	BE207855 bb06d06.x
	9	780.5	77.4	742	9	AU121735	AU121735 AU121735
	10	720	71.4	668	12	BM734828	BM734828 MONO1_13_
	11	688	68.3	1467	29	AY407187	AY407187 Homo sapi
	12	653	64.8	900	13	BQ948163	BQ948163 AGENCOURT
c	13	554	55.0	409	9	AI872457	AI872457 ty41g09.x
	14	528.5	52.4	1742	11	BC027251	BC027251 Mus muscu
	15	518.5	51.4	2728	11	AK028961	AK028961 Mus muscu
	16	518.5	51.4	2933	11	AK078769	AK078769 Mus muscu
	17	497.5	49.4	692	13	BY756731	BY756731 BY756731
	18	474	47.0	1219	29	AY407189	AY407189 Mus muscu
	19	469	46.5	794	9	AU124448	AU124448 AU124448
c	20	460.5	45.7	650	10	AW226598	AW226598 up09h09.x
c	21	427	42.4	329	9	AI206292	AI206292 qr26f06.x
	22	420	41.7	401	14	R80991	R80991 yi94c03.rl
c	23	405.5	40.2	652	10	AW226592	AW226592 up09g09.x
	24	396.5	39.3	423	10	BF563520	BF563520 UI-R-C4-a
c	25	393	39.0	383	13	C82712	C82712 C82712 rabb
	26	393	39.0	383	13	C83568	C83568 C83568 rabb
c	27	392.5	38.9	642	10	AW226573	AW226573 up09e09.x
	28	391.5	38.8	778	10	BF135381	BF135381 601783468
	29	390	38.7	1467	29	AY407188	AY407188 Pan trogl

BLANK SHEET(USPTO)

BLANK SHEET(USPTO)